

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTTGGGG
 TTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCCCCGAGTCTCAACCCTCAACTGTC
 ACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTCCCGGGAAGCCCCAGCACTGCC

GCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCA TAG CTG TCT GGC

S1		S5		S10		S15
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu						
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC						
216		225		234		243 252

	S20		S25		S29	1
Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu						
CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG						
261	270		279		288	297

	5		10		15
Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro					
GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC					
306	315		324		333 342

	20		25		30
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr					
CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC					
351	360		369		378 387

	35		40		45
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro					
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG					
396	405		414		423 432

	50		55		60
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr					
GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC					
441	450		459		468 477

	65		70		75
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys					
GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC					
486	495		504		513 522

	80		85		90
Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp					
CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC					
531	540		549		558 567

	95		100		105
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr					
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT					
576	585		594		603 612

	110		115		120
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu					
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC					
621	630		639		648 657

Fig.1/2

Asn.Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val
AAT GGG	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG
666		675			684			693			702		
		125					130				135		
Cys Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val
TGC ACC	TGC	CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC
711		720			729			738			747		
		140					145				150		
Ser Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys
TCC TGT	AGT	AAC	TGT	AAG	AAA	AGC	CTG	GAG	TGC	ACG	AAG	TTG	TGC
756		765			774			783			792		
		155					160				165		
Leu Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	Gly	Thr
CTA CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	ACT	GAG	GAC	TCA	GGC	ACC
801		810			819			828			837		
		170					175				180		
Thr Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	Leu
ACA GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	GGT	CTT	TGC	CTT	TTA
846		855			864			873			882		
		185					190				195		
Ser Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys
TCC CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	CAA	CGG	TGG	AAG
891		900			909			918			927		
		200					205				210		
Ser Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys
TCC AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	CCT	GAA	AAA
936		945			954			963			972		
		215					220				225		
Glu Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn
GAG GGG	GAG	CTT	GAA	GGA	ACT	ACT	ACT	AAG	CCC	CTG	GCC	CCA	AAC
981		990			999			1008			1017		
		230					235				240		
Pro Ser	Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe
CCA AGC	TTC	AGT	CCC	ACT	CCA	GGC	TTC	ACC	CCC	ACC	CTG	GGC	TTC
1026		1035			1044			1053			1062		
		245					250				255		
Ser Pro	Val	Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr
AGT CCC	GTG	CCC	AGT	TCC	ACC	TTC	ACC	TCC	AGC	TCC	ACC	TAT	ACC
1071		1080			1089			1098			1107		
		260					265				270		
Pro Gly	Asp	Cys	Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala
CCC GGT	GAC	TGT	CCC	AAC	TTT	GCG	GCT	CCC	CGC	AGA	GAG	GTG	GCA
1116		1125			1134			1143			1152		
		275					280				285		

Fig.1/3

Pro	Pro	Tyr	290	Gln	Gly	Ala	Asp	Pro	295	Ile	Leu	Ala	Thr	Ala	Leu	Ala
CCA	CCC	TAT		CAG	GGG	GCT	GAC	CCC		ATC	CTT	GCG	ACA	GCC	CTC	GCC
1161				1170				1179			1188			1197		
Ser	Asp	Pro	305	Ile	Pro	Asn	Pro	Leu	310	Gln	Lys	Trp	Glu	Asp	Ser	Ala
TCC	GAC	CCC		ATC	CCC	AAC	CCC	CTT		CAG	AAG	TGG	GAG	GAC	AGC	GCC
1206				1215				1224			1233			1242		
His	Lys	Pro	320	Gln	Ser	Leu	Asp	Thr	325	Asp	Asp	Pro	Ala	Thr	Leu	Tyr
CAC	AAG	CCA		CAG	AGC	CTA	GAC	ACT		GAT	GAC	CCC	GCG	ACG	CTG	TAC
1251				1260				1269			1278			1287		
Ala	Val	Val	335	Glu	Asn	Val	Pro	Pro	340	Leu	Arg	Trp				
GCC	GTG	GTG		GAG	AAC	GTG	CCC	CCG		TTG	CGC	TGG	AA	<u>GGAATTC</u>		
1296				1305				1314			1323			1332		

Fig.2

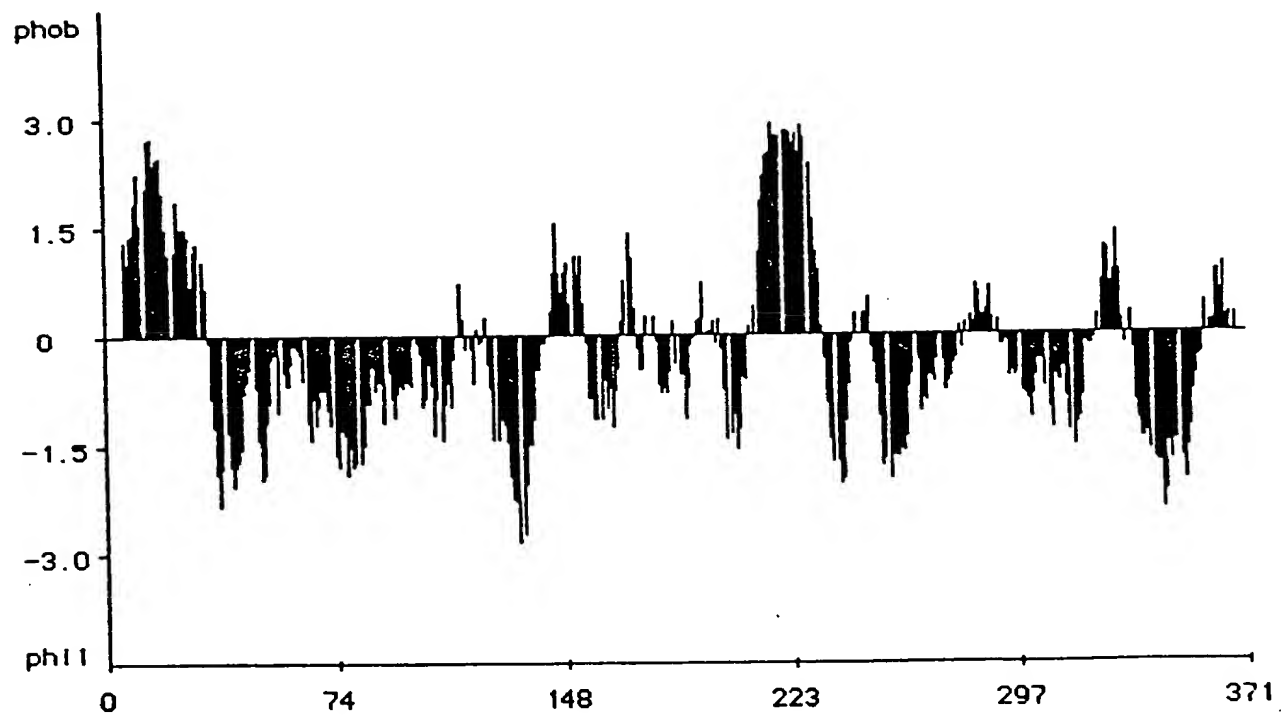


Fig.3

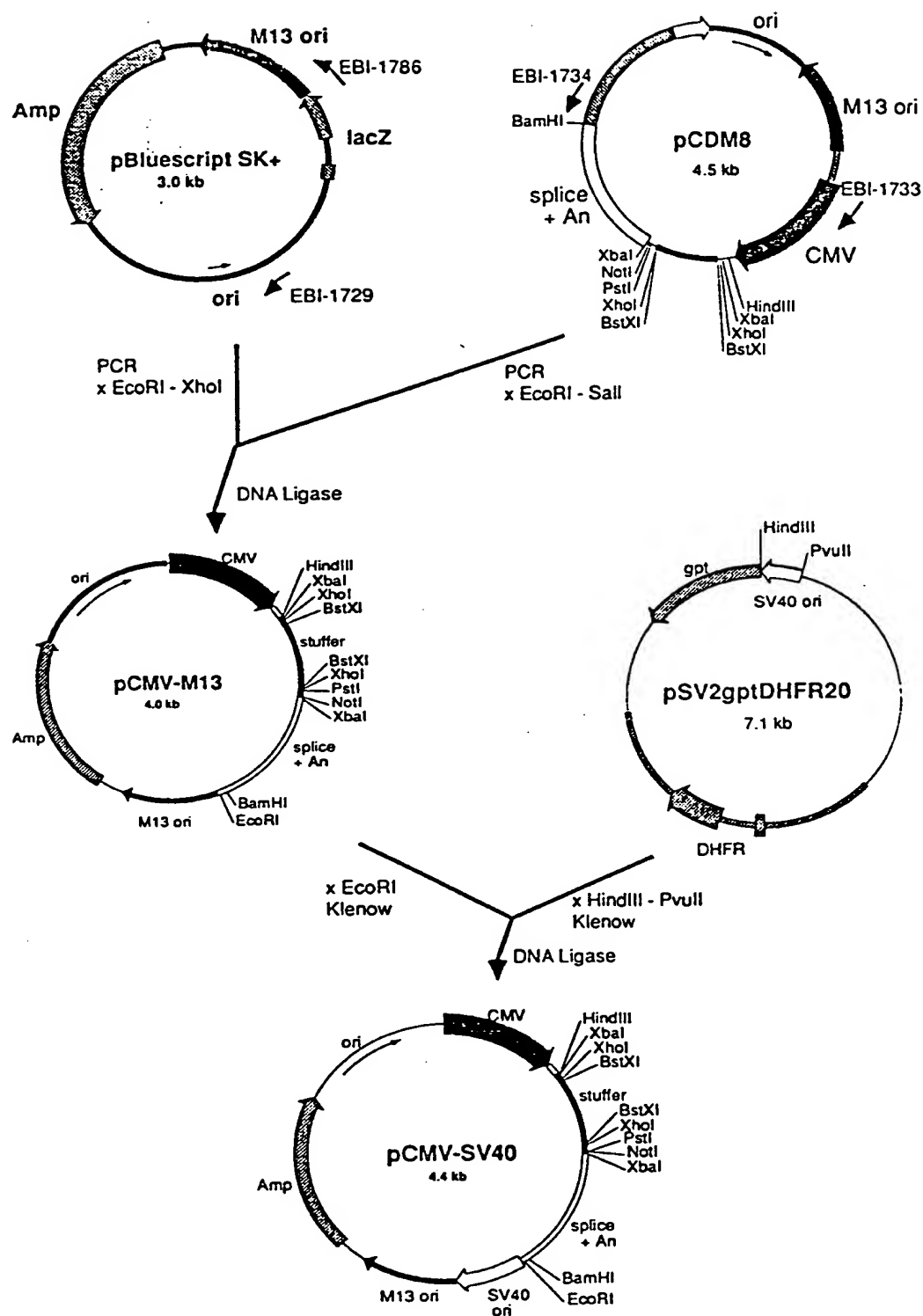


Fig.4

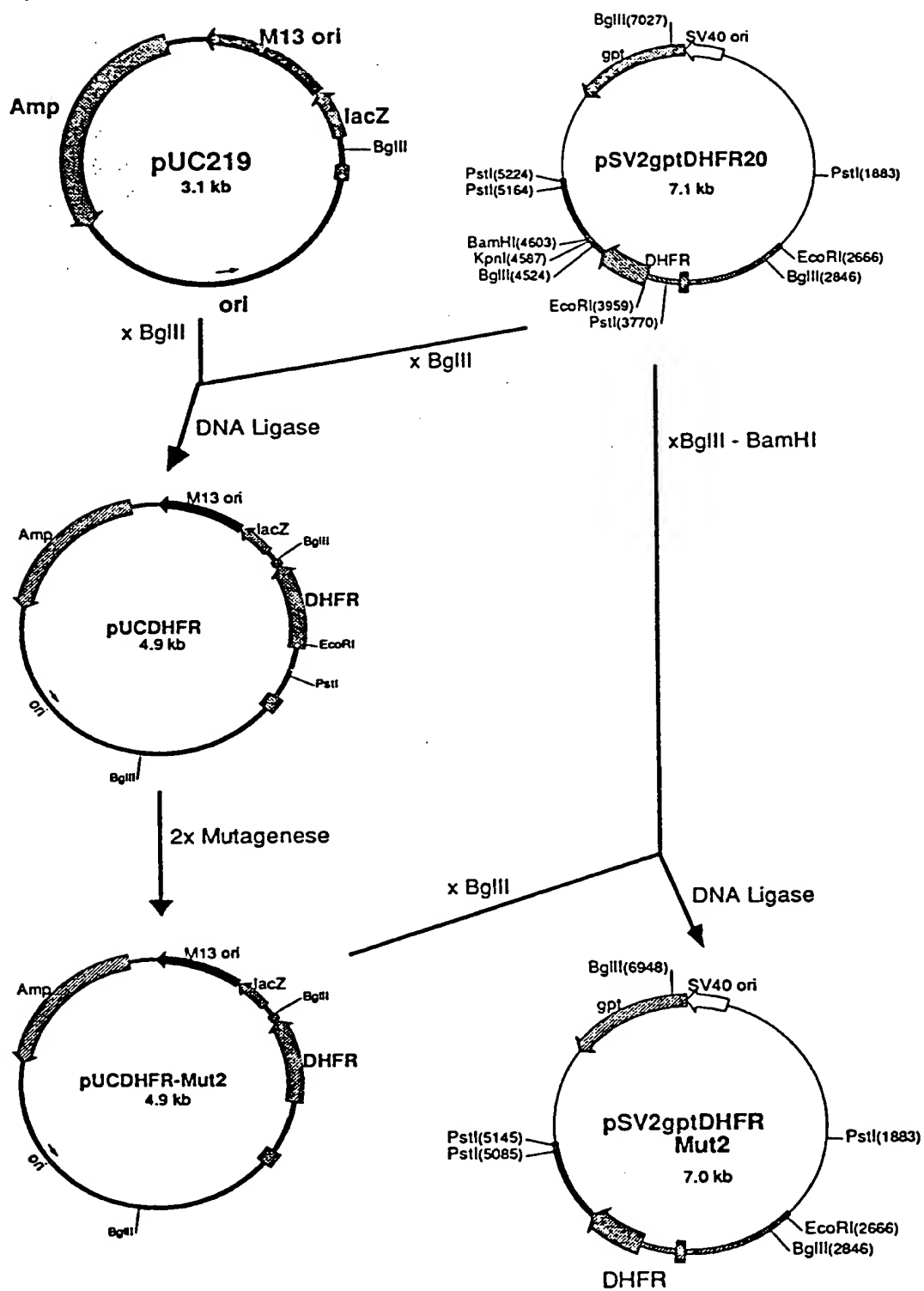


Fig.5

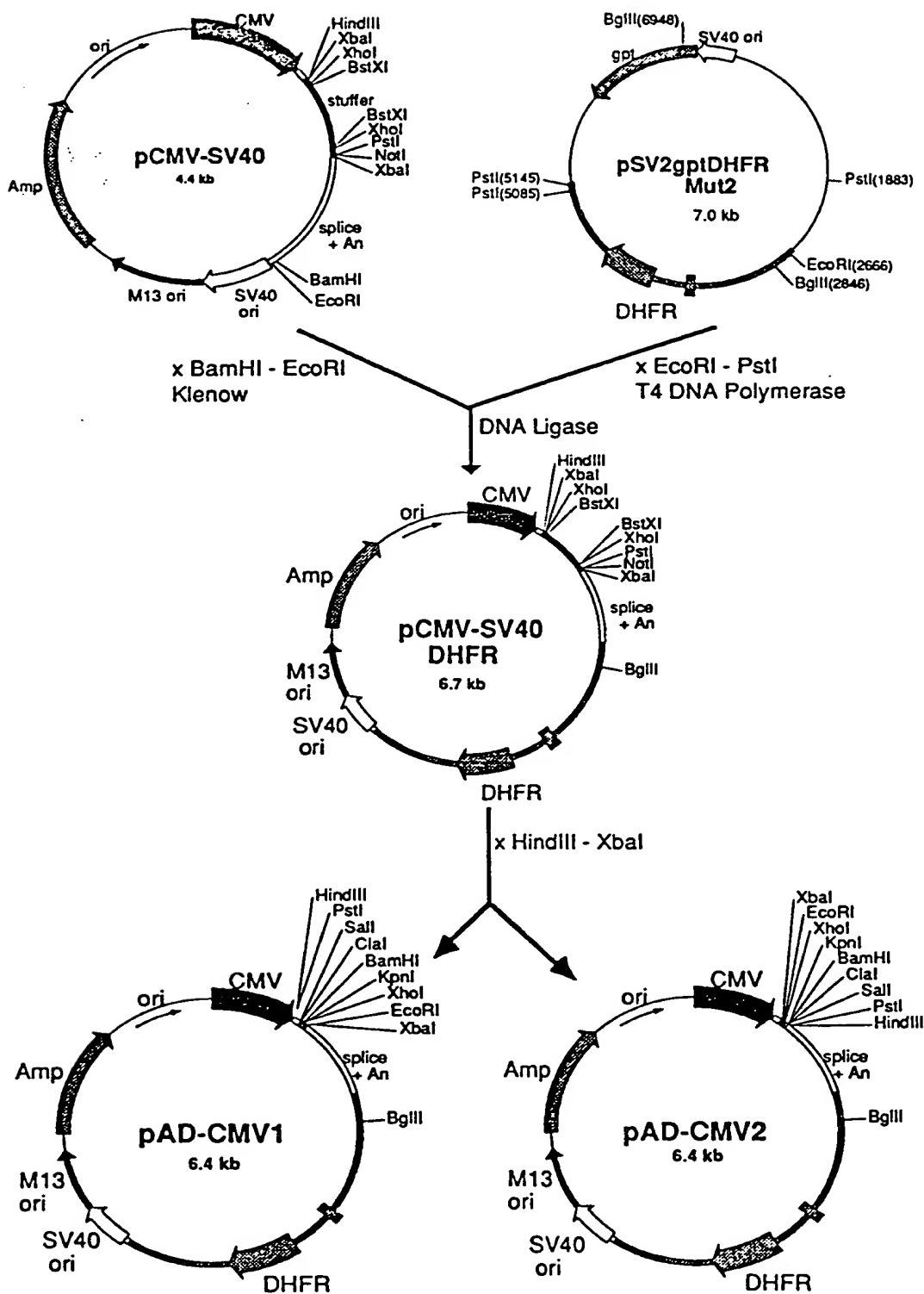


Fig.6/1

pAD-CMV1 : 6414 bp

TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT TAGTTCATAG	60
CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG GCTGACCGCC	120
CAACGACCCC CGCCCATTTGA CGTCAATAAT GACGTATGTT CCCATAGTAA CGCCAATAGG	180
GACTTTCCAT TGACGTCAAT GGGTGGAGTA TTTACGGTAA ACTGCCCCACT TGGCAGTACA	240
TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA AATGGCCCCG	300
CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT ACATCTACGT	360
ATTAGTCATC GCTATTACCA TGGTGATGCG GTTTTGGCAG TACATCAATG GGCCTGGATA	420
GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCATT GACGTCAATG GGAGTTTGTT	480
TTGGCACCAA AATCAACGGG ACTTTCAAA ATGTCGTAAC AACTCCGCC CATTGACGCA	540
AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC AGAGCTCTCT GGCTAACTAG	600
AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG	660
CTTCTGCAGG TCGACATCGA TGGATCCGGT ACCTCGAGCG CGAATTCTCT AGAGGATCTT	720
TGTGAAGGAA CCTTACTTCT GTGGTGTGAC ATAATTGGAC AACTACCTA CAGAGATTTA	780
AAGCTCTAAG GTAAATATAA AATTTTTAAG TGTATAATGT GTTAACTAC TGATTCTAAT	840
TGTTTGTGTA TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC	900
CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG ATGAGGCTAC	960
TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA	1020
CTTTCCTTCA GAATTGCTAA GTTTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC	1080
TTGCTTTGCT ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA	1140
AAAATATTTG ATGTATAGTG CCTTGACTAG AGATCATAAT CAGCCATACC ACATTTGTAG	1200
AGGTTTTACT TGCTTTAAAA AACCTCCCAC ACCTCCCCCT GAACCTGAAA CATAAAATGA	1260
ATGCAATTGT TGTGTTAAC TTGTTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA	1320
GCATCACAAA TTTCACAAAT AAAGCATTTT TTTCCTGCA TTCTAGTTGT GGTTTGTCCA	1380
AACTCATCAA TGTATCTTAT CATGTCTGGA TCAATTCTGA GAACTAGCC TTAAAGACAG	1440
ACAGCTTTGT TCTAGTCAGC CAGGCAAGCA TATGTAAATA AAGTTCCTCA GGGAAGTGA	1500
GTAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG AAGATTCCGC	1560
CTCAAGTTCC GGTTAACAAC AGGAGGCAAC GAGATCTCAA ATCTATTACT TCTAATCGGG	1620
TAATTAAAA CTTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG	1680
GCTCCGCCCT TCTCAGTACT CCCCACCATT AGGCTCGCTA CTCCACCTCC ACTTCCGGGC	1740

Fig.6/2

GCGACACCCA	CGTGCCCTCT	CCCACCCGAC	GCTAACCCCG	CCCCTGCCCC	TCTGACCCCG	1800
CCCACCACCT	GGCCCCGCCC	CGTTGAGGAC	AGAAGAAACC	CCGGGCAGCC	GCAGCCAAGG	1860
CGGACGGGTA	GACGCTGGGG	GCGCTGAGGA	GTCGTCTCT	ACCTTCTCTG	CTGGCTCGGT	1920
GGGGGACGCG	GTGGATCTCA	GGCTTCCGGA	AGACTGGAAG	AACCGGCTCA	GAACCGCTTG	1980
TCTCCGCGGG	GCTTGGGCGG	CGGAAGAATG	GCCGCTAGAC	GCGGACTTGG	TGCGAGGCAT	2040
CGCAGGATGC	AGAAGAGCAA	GCCCCCGGGG	AGCGCGCGGC	TGTACTACCC	CGCGCCTGGA	2100
GCGGCCACGC	CGGACTGGGC	GGGGCCGGCC	TGGTGGAGGC	GGAGTCTGAC	CTCGTGGAGG	2160
CGGGGCCTCT	GATGTTCAAA	TAGGATGCTA	GGCTTGTTGA	GGCGTGGCCT	CCGATTCACA	2220
AGTGGGAAGC	AGCGCCGGGC	GACTGCAATT	TCGCGCCAAA	CTTGGGGGAA	GCACAGCGTA	2280
CAGGCTGCCT	AGGTGATCGC	TGCTGCTGTC	ATGGTTCGAC	CGCTGAACTG	CATCGTCGCC	2340
GTGTCCCAGA	ATATGGGCAT	CGGCAAGAAC	GGAGACCTTC	CCTGGCCAAT	GCTCAGGTAC	2400
TGGCTGGATT	GGGTTAGGGA	AACCGAGGCG	GTTGCTGAA	TCGGGTCGAG	CACTTGGCGG	2460
AGACGCGCGG	GCCAACTACT	TAGGGACAGT	CATGAGGGGT	AGGCCCGCCG	GCTGCTGCCC	2520
TTGCCCATGC	CCGCGGTGAT	CCCCATGCTG	TGCCAGCCTT	TGCCCAGAGG	CGCTCTAGCT	2580
GGGAGCAAAG	TCCGGTCACT	GGGCAGCACC	ACCCCCCGGA	CTTGCAATGGG	TAGCCGCTGA	2640
GATGGAGCCT	GAGCACACGT	GACAGGGTCC	CTGTTAACGC	AGTGTTTCTC	TAACCTTCAG	2700
GAACGAGTTC	AAGTACTTCC	AAAGAATGAC	CACCACCTCC	TCAGTGGAAG	GTAAACAGAA	2760
CCTGGTGATT	ATGGGCCGGA	AAACCTGGTT	CTCCATTCTC	GAGAAGAATC	GACCTTTAAA	2820
GGACAGAATT	AATATAGTTC	TCAGTAGAGA	GCTCAAGGAA	CCACCACAAG	GAGCTCATTT	2880
TCTTGCCAAA	AGTCTGGACC	ATGCCTTAAA	ACTTATTGAA	CAACCAGAGT	TAGCAGATAA	2940
AGTGGACATG	GTTTGGATAG	TTGGAGGCAG	TTCCGTTTAC	AAGGAAGCCA	TGAATCAGCC	3000
AGGCCATCTC	AGACTCTTTG	TGACAAGGAT	CATGCAGGAA	TTTGAAAGTG	ACACGTTCTT	3060
CCCAGAAATT	GATTTGGAGA	AATATAAACT	TCTCCCAGAG	TACCCAGGGG	TCCTTTCTGA	3120
AGTCCAGGAG	GAAAAAGGCA	TCAAGTATAA	ATTTGAAGTC	TATGAGAAGA	AAGGCTAACA	3180
GAAAGATACT	TGCTGATTGA	CTTCAAGTTC	TACTGCTTTC	CTCCTAAAAT	TATGCATTTT	3240
TACAAGACCA	TGGGACTTGT	GTTGGCTTTA	GATCCTGTGC	ATCCTGGGCA	ACTGTTGTAC	3300
TCTAAGCCAC	TCCCCAAAGT	CATGCCCCAG	CCCCTGTATA	ATTCTAAACA	ATTAGAATTA	3360
TTTTCATTTT	CATTAGTCTA	ACCAGGTTAT	ATTAAATATA	CTTTAAGAAA	CACCATTTCG	3420
CATAAAGTTC	TCAATGCCCC	TCCCATGCAG	CCTCAAGTGG	CTCCCCAGCA	GATGCATAGG	3480
GTAGTGTGTG	TACAAGAGAC	CCCAAAGACA	TAGAGCCCCT	GAGAGCATGA	GCTGATATGG	3540

Fig.6/3

GGGCTCATAG AGATAGGAGC TAGATGAATA AGTACAAAGG GCAGAAATGG GTTTTAACCA	3600
GCAGAGCTAG' AACTCAGACT TTAAAGAAAA TTAGATCAAA GTAGAGACTG AATTATTCTG	3660
CACATCAGAC TCTGAGCAGA GTTCTGTTCA CTCAGACAGA AAATGGGTAA ATTGAGAGCT	3720
GGCTCCATTG TGCTCCTTAG AGATGGGAGC AGGTGGAGGA TTATATAAGG TCTGGAACAT	3780
TTAACTTCTC CGTTTCTCAT CTTCAGTGAG ATTCCAAGGG ATACTACAAT TCTGTGGAAT	3840
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC	3900
ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA	3960
AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC	4020
ATCCCGCCCC TAACTCCGCC CAGTTCCGCC CATCTCCGC CCCATGGCTG ACTAATTTTT	4080
TTTATTTATG CAGAGGCCGA GCGCCTCTG AGCTATTCCA GAAGTAGTGA GGAGGCTTTT	4140
TTGGAGGCCT AGGCTTTTGC AAAAAAGCTA ATTCAGCCTG AATGGCGAAT GGGACGCGCC	4200
CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT	4260
TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG CCACGTTTCG	4320
CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT	4380
ACGGCACCTC GACCCCAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC	4440
TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG	4500
TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTGTATTT ATAAGGGATT	4560
TTGCCGATTT CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT	4620
TTTAACAAAA TATTAACGTT TACAATTTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA	4680
ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA	4740
CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT	4800
GTCGCCCTTA TTCCCTTTTT TGCGGCATT TGCCTTCCTG TTTTGTCTCA CCCAGAAACG	4860
CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG	4920
GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG	4980
AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG	5040
CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA	5100
GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG	5160
AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC	5220
GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG	5280
AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG	5340

TTGCGCAAAC TATTAAGTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC	5400
TGGATGGAGG' CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG	5460
TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG	5520
GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT	5580
ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA	5640
CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACTTCA TTTTAAATTT	5700
AAAAGGATCT AGGTGAAGAT CCTTTTGTAT AATCTCATGA CCAAAATCCC TTAACGTGAG	5760
TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT	5820
TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT	5880
TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG	5940
CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT	6000
GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC	6060
GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG	6120
TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA	6180
CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG	6240
GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG	6300
GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA	6360
TTTTTGATGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCC	

Fig.7A

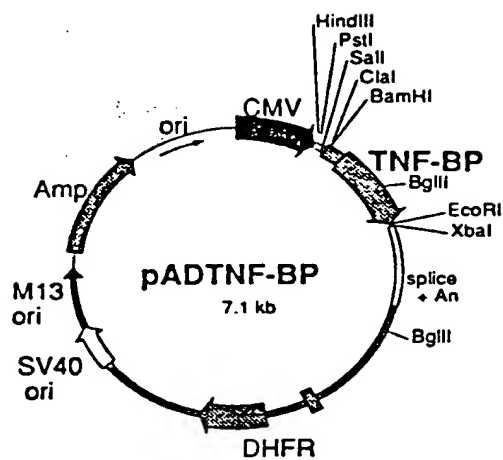


Fig.7B

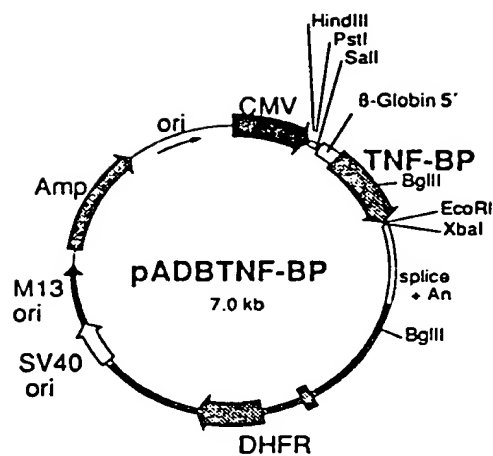


Fig.7C

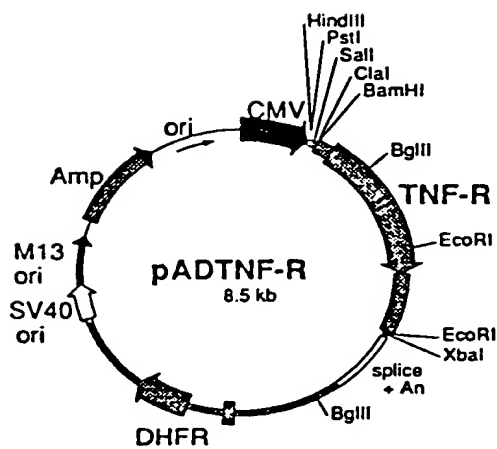


Fig.7D

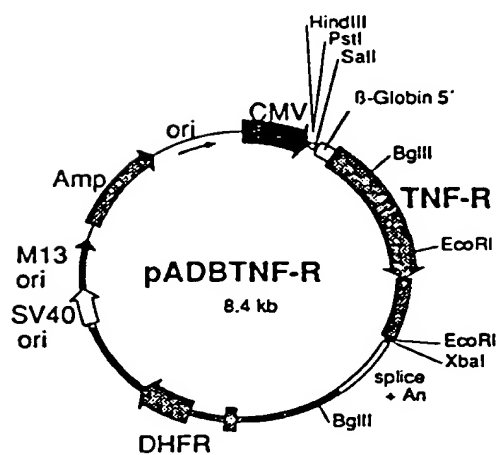


Fig.8/1

raTNF-R

GAATTCCTTT	TCTCCGAGTT	TTCTGAACTC	TGGCTCATGA	TCGGGCTTAC	TGGATACGAG	60
AATCCTGGAG	GACCGTACCC	TGATTTCCAT	CTACCTCTGA	CTTTGAGCCT	TTCTAACCCG	120
GGGCTCACGC	TGCCAACACC	CGGGCCACCT	GGTCCGATCG	TCTTACTTCA	TTCACCAGCG	180
TTGCCAATTG	CTGCCCTGTC	CCCAGCCCCA	ATGGGGGAGT	GAGAGAGGCC	ACTGCCGGCC	240

GGAC

245/1	275/11
ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG	
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu Ala Leu Leu Met	
305/21	335/31
GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG	
Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg	
365/41	395/51
GAT AAT TTG TGT CCC CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC	
Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr	
425/61	455/71
AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC	
Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val	
485/81	515/91
TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC	
Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu	
545/101	575/111
AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC	
Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp	
605/121	635/131
ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT	
Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His	
665/141	695/151
TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG	
Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu	
725/161	755/171
AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC	
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr	
785/181	815/191
CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA	
Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala	
845/201	875/211
AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA	
Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu	
905/221	935/231
GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG	
Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg	
965/241	995/251
CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA	
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu	
1025/261	1055/271
GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC	
Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly	
1085/281	1115/291
TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC	
Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr	
1145/301	1175/311
CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG	
Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu	
1205/321	1235/331
GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC	
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile	
1265/341	1295/351
CCC GCC CCT GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT	

Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
 1325/361 1355/371
 GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG
 Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu
 1385/381 1415/391
 TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG
 Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly
 1445/401 1475/411
 CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA
 Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
 1505/421 1535/431
 CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC
 His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys
 1565/441 1595/451
 CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG
 Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro
 1625/461
 CGA TAA
 Arg Stop
 GGCCACACCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT 1680
 GCCCTGCTTC CCTGTGAACC TCCTCTTTGG TCCTCTAGGG GGCAGGCTCG ATCTGGCAGG 1740
 CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGGT GTACATAGCT TTTCCCAGCT 1800
 GCCGAGGACA GCCTGTGCCA GCCACTTGTG CATGGCAGGG AAGTGTGCCA TCTGCTCCCA 1860
 GACAGCTGAG GGTGCCAAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT 1920
 GATACCCACT TGGGATGCAA GGACCCAAAC AAAGCTTCTC AGGGCCTCCT CAGTTGATTT 1980
 CTGGGCCCTT TTCACAGTAG ATAAACAGT CTTTGTATTG ATTATATCAC ACTAATGGAT 2040
 GAACGGTTGA ACTCCCTAAG GTAGGGGCAA GCACAGAACA GTGGGGTCTC CAGCTGGAGC 2100
 CCCCAGCTCT TGTAATACA CTAAAAATCT AAAAGTGAAA AAAAAAAAAA AAAAAAAAAA 2160
 AAAAAAGGAA TTC

Fig.9/1

huTNF-R

GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC TGGGACCAGG 60
 CCGTGATCTC TATGCCCAG TCTCAACCCT CAACTGTCAC CCCAAGGCAC TTGGGACGTC 120
 CTGGACAGAC CGAGTCCCGG GAAGCCCCAG CACTGCCGCT GCCACACTGC CCTGAGCCCCA 180
 AATGGGGGAG TGAGAGGCCA TAGCTGTCTG GC

213/1	243/11
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG	CTG CCA CTG GTG CTC CTG GAG CTG TTG GTG
Met Gly Leu Ser Thr Val Pro Asp Leu Leu	Leu Pro Leu Val Leu Leu Glu Leu Leu Val
273/21	303/31
GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG	GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA
Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu	Val Pro His Leu Gly Asp Arg Glu Lys Arg
333/41	363/51
GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC	CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile	His Pro Gln Asn Asn Ser Ile Cys Cys Thr
393/61	423/71
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT	GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn	Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
453/81	483/91
TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC	GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr	Ala Ser Glu Asn His Leu Arg His Cys Leu
513/101	543/111
AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT	CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC
Ser Cys Ser Lys Cys Arg Lys Glu Met Gly	Gln Val Glu Ile Ser Ser Cys Thr Val Asp
573/121	603/131
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC	CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn	Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu
633/141	663/151
TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC	AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG
Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu	Asn Gly Thr Val His Leu Ser Cys Gln Glu
693/161	723/171
AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA	GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC
Lys Gln Asn Thr Val Cys Thr Cys His Ala	Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
753/181	783/191
TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG	TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu	Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
813/201	843/211
AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC	ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT
Asn Val Lys Gly Thr Glu Asp Ser Gly Thr	Thr Val Leu Leu Pro Leu Val Ile Phe Phe
873/221	903/231
GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT	GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG
Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile	Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
933/241	963/251
TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA	TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys	Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu
993/261	1023/271
GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC	CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC
Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn	Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr
1053/281	1083/291
CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT	TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser	Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1113/301	1143/311
CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC	CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro	Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
1173/321	1203/331
GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC	TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala	Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys

Fig.9/2

B/484312

1233/341
 TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC
 Trp Glu Asp Ser Ala His Lys Pro Gln Ser
 1293/361
 GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC
 Ala Val Val Glu Asn Val Pro Pro Leu Arg
 1353/381
 AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG
 Ser Asp His Glu Ile Asp Arg Leu Glu Leu
 1413/401
 TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg
 1473/421
 CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG
 Leu Gly Arg Val Leu Arg Asp Met Asp Leu
 1533/441
 CTT TGC GGC CCC GCC GCC CTC CCG CCC GCG
 Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg Stop

1263/351
 CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC
 Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
 1323/371
 TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG
 Trp Lys Glu Phe Val Arg Arg Leu Gly Leu
 1383/391
 CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA
 Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
 1443/411
 ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG
 Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
 1503/431
 CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG
 Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala
 1563/451
 CTT CTT CTC AGA TGA
 1580

1620
 GGCTGCGCCC CTGCGGGCAG CTCTAAGGAC CGTCCTGCGA
 GATCGCCTTC CAACCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG 1680
 CTAGCAGCCG CCTACTTGGT GCTAACCCT CGATGTACAT AGCTTTTCTC AGCTGCCTGC 1740
 GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT 1800
 GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTGG GGTGTCCTCA 1860
 CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC CTTTTTCACA GTGCATAAGC 1920
 AGTTTTTTTT GTTTTGTGTT TGTTTTGTTT TGTTTTTAAA TCAATCATGT TACACTAATA 1980
 GAAACTTGGC ACTCCTGTGC CCTCTGCCTG GACAAGCACA TAGCAAGCTG AACTGTCCTA 2040
 AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA 2100
 CACTAAAATT CTGAAGTTAA AAAAAAAAAA AAAAGGAATT C 2141

Fig.10

